

#4

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/517,309  
Source: PCT  
Date Processed by STIC: 10/28/2005

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PCT

## RAW SEQUENCE LISTING

DATE: 10/28/2005

PATENT APPLICATION: US/10/517,309

TIME: 10:15:42

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Output Set: N:\CRF4\10282005\J517309.raw

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3 <110> APPLICANT: MIRAS, STEPHANE
4     SALVI, DANIEL
5     ROLLAND, NORBERT
6     JOYARD, JACQUES
7     FERRO, MYRIAM
8     GARIN, JEROME
9     GRUNWALD, DIDIER
11 <120> TITLE OF INVENTION: PLASTIDAL TARGETING PEPTIDE
13 <130> FILE REFERENCE: 263270USPCT
15 <140> CURRENT APPLICATION NUMBER: 10/517,309
C--> 16 <141> CURRENT FILING DATE: 2004-12-17
18 <150> PRIOR APPLICATION NUMBER: PCT/FR03/01877
19 <151> PRIOR FILING DATE: 2003-06-19
21 <150> PRIOR APPLICATION NUMBER: FR02/07729
22 <151> PRIOR FILING DATE: 2002-06-21
24 <160> NUMBER OF SEQ ID NOS: 18
26 <170> SOFTWARE: PatentIn version 3.3
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29 <211> LENGTH: 329
30 <212> TYPE: PRT
31 <213> ORGANISM: Arabidopsis thaliana
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40           20           25           30
43 Ser Asn Glu Val Cys Leu Lys Leu Glu Ala Thr Ser Leu Asn Pro Val
44           35           40           45
47 Asp Trp Lys Ile Gln Lys Gly Met Ile Arg Pro Phe Leu Pro Arg Lys
48           50           55           60
51 Phe Pro Cys Ile Pro Ala Thr Asp Val Ala Gly Glu Val Val Glu Val
52 65           70           75           80
55 Gly Ser Gly Val Lys Asn Phe Lys Ala Gly Asp Lys Val Val Ala Val
56           85           90           95
59 Leu Ser His Leu Gly Gly Gly Gly Leu Ala Glu Phe Ala Val Ala Thr
60           100          105          110
63 Glu Lys Leu Thr Val Lys Arg Pro Gln Glu Val Gly Ala Ala Glu Ala
64           115          120          125
67 Ala Ala Leu Pro Val Ala Gly Leu Thr Ala Leu Gln Ala Leu Thr Asn
68           130          135          140
71 Pro Ala Gly Leu Lys Leu Asp Gly Thr Gly Lys Lys Ala Asn Ile Leu
72 145          150          155          160
75 Val Thr Ala Ala Ser Gly Gly Val Gly His Tyr Ala Val Gln Leu Ala

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79 Lys Leu Ala Asn Ala His Val Thr Ala Thr Cys Gly Ala Arg Asn Ile
80          180          185          190
83 Glu Phe Val Lys Ser Leu Gly Ala Asp Glu Val Leu Asp Tyr Lys Thr
84          195          200          205
87 Pro Glu Gly Ala Ala Leu Lys Ser Pro Ser Gly Lys Lys Tyr Asp Ala
88          210          215          220
91 Val Val His Cys Ala Asn Gly Ile Pro Phe Ser Val Phe Glu Pro Asn
92 225          230          235          240
95 Leu Ser Glu Asn Gly Lys Val Ile Asp Ile Thr Pro Gly Pro Asn Ala
96          245          250          255
99 Met Trp Thr Tyr Ala Val Lys Lys Ile Thr Met Ser Lys Lys Gln Leu
100          260          265          270
103 Val Pro Leu Leu Leu Ile Pro Lys Ala Glu Asn Leu Glu Phe Met Val
104          275          280          285
107 Asn Leu Val Lys Glu Gly Lys Val Lys Thr Val Ile Asp Ser Lys His
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129 ttcaatattc tggctatggt ggtggaactg atgcttttaa gcatgttgaa gttgctgttc      180
131 ctgatccaaa gtctgatgag ttattgctta aaattgaggc tgcaactttg aacccaattg      240
133 attggaagat tcagaagggt gtacttcgtc ccctcttacc ccgcaagttc cctactatac      300
135 ctggaactga tgttgctggg gaggtagtc aggctggatc tgctgtaaat aggtttaaaa      360
137 ctggtgacaa agtcgtggcc gtgcttagtc atgctactgg ggggtgacta gctgaatatg      420
139 ccgtggcgaa ggagaacctg acagttgcta gaccaccaga agtatcagca gcagaagggtg      480
141 ctgccttacc tgttgctgcc ctacggctc accaagctct caccagttt gccaacatca      540
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145 gccactatgc ggtccagctg gcaaagctcg ggaacacgca tgtaacagca acatgtggag      660
147 cccgcaacct agatttcgtg aaaggcttgg gtgccgatga ggttcttgac taaaaaacac      720
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166 1          5          10          15

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173 Ser Asp Glu Leu Leu Lys Ile Glu Ala Ala Thr Leu Asn Pro Ile
174      35      40      45
177 Asp Trp Lys Ile Gln Lys Gly Val Leu Arg Pro Leu Leu Pro Arg Lys
178      50      55      60
181 Phe Pro Thr Ile Pro Gly Thr Asp Val Ala Gly Glu Val Val Gln Ala
182 65      70      75      80
185 Gly Ser Ala Val Asn Arg Phe Lys Thr Gly Asp Lys Val Val Ala Val
186      85      90      95
189 Leu Ser His Ala Thr Gly Gly Ala Leu Ala Glu Tyr Ala Val Ala Lys
190      100     105     110
193 Glu Asn Leu Thr Val Ala Arg Pro Pro Glu Val Ser Ala Ala Glu Gly
194      115     120     125
197 Ala Ala Leu Pro Val Ala Ala Leu Thr Ala His Gln Ala Leu Thr Gln
198      130     135     140
201 Phe Ala Asn Ile Lys Leu Asp Gly Ser Gly Glu Arg Lys Asn Ile Leu
202 145     150     155     160
205 Ile Thr Ala Ala Ser Gly Gly Val Gly His Tyr Ala Val Gln Leu Ala
206      165     170     175
209 Lys Leu Gly Asn Thr His Val Thr Ala Thr Cys Gly Ala Arg Asn Leu
210      180     185     190
213 Asp Phe Val Lys Gly Leu Gly Ala Asp Glu Val Leu Asp Tyr Lys Thr
214      195     200     205
217 Pro Glu Gly Ala Ser Leu Thr Ser Pro Ser Gly Lys Lys Tyr Asp Tyr
218      210     215     220
221 Val Val His Gly Ala Ser Gly Ile Pro Trp Ser Thr Phe Glu Pro Asn
222 225     230     235     240
225 Leu Ser Glu Ala Gly Lys Val Ile Asp Leu Thr Pro Gly Pro Thr Ala
226      245     250     255
229 Met Met Thr Phe Ala Trp Lys Lys Leu Thr Phe Ser Lys Lys Gln Leu
230      260     265     270
233 Val Pro Leu Leu Leu Ile Pro Lys Ile Pro Asn Phe Glu Tyr Val Val
234      275     280     285
237 Asn Leu Val Lys Glu Lys Lys Leu Lys Thr Val Ile Asp Ser Lys His
238      290     295     300
241 Pro Leu Ser Lys Gly Glu Asp Ala Trp Ser Arg Ile Met Gly Gly His
242 305     310     315     320
245 Ala Thr Gly Lys Ile Ile Ile Glu Pro
246      325
249 <210> SEQ ID NO: 4
250 <211> LENGTH: 61
251 <212> TYPE: PRT
252 <213> ORGANISM: Arabidopsis thaliana
254 <400> SEQUENCE: 4
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257 1      5      10      15
260 Met Ile Arg Pro Phe Leu Pro Arg Lys Phe Pro Cys Ile Pro Ala Thr
261      20      25      30

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264 Asp Val Ala Gly Glu Val Val Glu Val Gly Ser Gly Val Lys Asn Phe
265          35          40          45
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273 <211> LENGTH: 61
274 <212> TYPE: PRT
275 <213> ORGANISM: Spinacia oleracea
277 <400> SEQUENCE: 5
279 Ile Glu Ala Ala Thr Leu Asn Pro Ile Asp Trp Lys Ile Gln Lys Gly
280 1          5          10          15
283 Val Leu Arg Pro Leu Leu Pro Arg Lys Phe Pro Thr Ile Pro Gly Thr
284          20          25          30
287 Asp Val Ala Gly Glu Val Val Gln Ala Gly Ser Ala Val Asn Arg Phe
288          35          40          45
291 Lys Thr Gly Asp Lys Val Val Ala Val Leu Ser His Ala
292          50          55          60
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297 <212> TYPE: PRT
298 <213> ORGANISM: Escherichia coli
300 <400> SEQUENCE: 6
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306 Gln Ala Val Glu Phe Thr Pro Ala Asp Pro Ala Glu Asn Glu Ile Gln
307          20          25          30
310 Val Glu Asn Lys Ala Ile Gly Ile Asn Phe Ile Asp Thr Tyr Ile Arg
311          35          40          45
314 Ser Gly Leu Tyr Pro Pro Pro Ser Leu Pro Ser Gly Leu Gly Thr Glu
315          50          55          60
318 Ala Ala Gly Ile Val Ser Lys Val Gly Ser Gly Val Lys His Ile Lys
319 65          70          75          80
322 Ala Gly Asp Arg Val Val Tyr Ala Gln Ser Ala Leu Gly Ala Tyr Ser
323          85          90          95
326 Ser Val His Asn Ile Ile Ala Asp Lys Ala Ala Ile Leu Pro Ala Ala
327          100         105         110
330 Ile Ser Phe Glu Gln Ala Ala Ala Ser Phe Leu Lys Gly Leu Thr Val
331          115         120         125
334 Tyr Tyr Leu Leu Arg Lys Thr Tyr Glu Ile Lys Pro Asp Glu Gln Phe
335          130         135         140
338 Leu Phe His Ala Ala Ala Gly Gly Val Gly Leu Ile Ala Cys Gln Trp
339 145          150         155         160
342 Ala Lys Ala Leu Gly Ala Lys Leu Ile Gly Thr Val Gly Thr Ala Gln
343          165         170         175
346 Lys Ala Gln Ser Ala Leu Lys Ala Gly Ala Trp Gln Val Ile Asn Tyr
347          180         185         190
350 Arg Glu Glu Asp Leu Val Glu Arg Leu Lys Glu Ile Thr Gly Gly Lys
351          195         200         205
354 Lys Val Arg Val Val Tyr Asp Ser Val Gly Arg Asp Thr Trp Glu Arg

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Input Set : D:\263270US.txt

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355      210      215      220
358 Ser Leu Asp Cys Leu Gln Arg Arg Gly Leu Met Val Ser Phe Gly Asn
359 225      230      235      240
362 Ser Ser Gly Ala Val Thr Gly Val Asn Leu Gly Ile Leu Asn Gln Lys
363      245      250      255
366 Gly Ser Leu Tyr Val Thr Arg Pro Ser Leu Gln Gly Tyr Ile Thr Thr
367      260      265      270
370 Arg Glu Glu Leu Thr Glu Ala Ser Asn Glu Leu Phe Ser Leu Ile Ala
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377 <213> ORGANISM: Saccharomyces cerevisiae
379 <400> SEQUENCE: 7
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386      20      25      30
389 Ile Ser Glu Glu Leu Leu Ile Lys Asn Lys Tyr Thr Gly Val Asn
390      35      40      45
393 Tyr Ile Glu Ser Tyr Phe Arg Lys Gly Ile Tyr Pro Cys Glu Lys Pro
394      50      55      60
397 Tyr Val Leu Gly Arg Glu Ala Ser Gly Thr Val Val Ala Lys Gly Lys
398 65      70      75      80
401 Gly Val Thr Asn Phe Glu Val Gly Asp Gln Val Ala Tyr Ile Ser Asn
402      85      90      95
405 Ser Thr Phe Ala Gln Tyr Ser Lys Ile Ser Ser Gln Gly Pro Val Met
406      100     105     110
409 Lys Leu Pro Lys Gly Thr Ser Asp Glu Glu Leu Lys Leu Tyr Ala Ala
410      115     120     125
413 Gly Leu Leu Gln Val Leu Thr Ala Leu Ser Phe Thr Asn Glu Ala Tyr
414      130     135     140
417 His Val Lys Lys Gly Asp Tyr Val Leu Leu Phe Ala Ala Ala Gly Gly
418 145     150     155     160
421 Val Gly Leu Ile Leu Asn Gln Leu Leu Lys Met Lys Gly Ala His Thr
422      165     170     175
425 Ile Ala Val Ala Ser Thr Asp Glu Lys Leu Lys Ile Ala Lys Glu Tyr
426      180     185     190
429 Gly Ala Glu Tyr Leu Ile Asn Ala Ser Lys Glu Asp Ile Leu Arg Gln
430      195     200     205
433 Val Leu Lys Phe Thr Asn Gly Lys Gly Val Asp Ala Ser Phe Asp Ser
434      210     215     220
437 Val Gly Lys Asp Thr Phe Glu Ile Ser Leu Ala Ala Leu Lys Arg Lys
438 225     230     235     240
441 Gly Val Phe Val Ser Phe Gly Asn Ala Ser Gly Leu Ile Pro Pro Phe
442      245     250     255
445 Ser Ile Thr Arg Leu Ser Pro Lys Asn Ile Thr Leu Val Arg Pro Gln
446      260     265     270
449 Leu Tyr Gly Tyr Ile Ala Asp Pro Glu Glu Trp Lys Tyr Tyr Ser Asp

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VERIFICATION SUMMARY

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